In the claims:

1.-2. (cancelled)

3. (withdrawn) The oligonucleotide library of claim 1, wherein said transcriptome is a rat transcriptome.

4. (withdrawn) The oligonucleotide library of claim 1, wherein said transcriptome is a mouse transcriptome.

5.-15. (cancelled)

16. (withdrawn) A method for expression profiling a cell or tissue sample that contains two or more RNAs of various abundances, comprising measuring hybridization signals of said sample to a plurality of oligonucleotide sequences, thereby determining the levels of said two or more RNAs in said sample and, where a RNA is transcribed from a transcription unit that has a set of splice variants, determining the total level of the set of splice variants, wherein said plurality is provided by the oligonucleotide library of claim 1 or a subset thereof.

17. (withdrawn) The method of claim 16, wherein said hybridization signals are obtained from a nucleotide chip.

18. (withdrawn) The method of claim 16, wherein said hybridization signals are obtained from an electrophoresis gel.

19. (withdrawn) A method for expression profiling a cell or tissue sample that contains two or more RNAs of various abundances, comprising measuring hybridization signals of said sample to a plurality of oligonucleotide sequences, thereby determining the levels of said two or more RNAs in said sample

and, where a RNA is transcribed from a transcription unit that has a set of splice variants, determining the total level of the set of splice variants, wherein said plurality is provided by the oligonucleotide library of claim 5 or a subset thereof.

20. (withdrawn) The method of claim 19, wherein said hybridization signals are obtained from a nucleotide chip.

21. (withdrawn) The method of claim 19, wherein said hybridization signals are obtained from an electrophoresis gel.

22. (withdrawn) A method for expression profiling a cell or tissue sample that contains two or more RNAs of various abundances, comprising measuring hybridization signals of said sample to a plurality of oligonucleotide sequences, thereby determining the levels of said two or more RNAs in said sample and, where a RNA is transcribed from a transcription unit that has a set of splice variants, determining the total level of the set of splice variants, wherein said plurality is provided by the oligonucleotide library of claim 6 or a subset thereof.

23. (withdrawn) The method of claim 22, wherein said hybridization signals are obtained from a nucleotide chip.

24. (withdrawn) The method of claim 22, wherein said hybridization signals are obtained from an electrophoresis gel.

25. (withdrawn) A method for expression profiling a cell or tissue sample that contains two or more RNAs of various abundances, comprising measuring hybridization signals of said sample to a plurality of oligonucleotide sequences, thereby determining the levels of said two or more RNAs in said sample and, where a RNA is transcribed from a transcription unit that has a set of splice

variants, determining the total level of the set of splice variants, wherein said plurality is provided by the oligonucleotide library of claim 8 or a subset thereof.

26. (withdrawn) The method of claim 25, wherein said hybridization signals are obtained from a nucleotide chip.

27. (withdrawn) The method of claim 25, wherein said hybridization signals are obtained from an electrophoresis gel.

28. (withdrawn) A method for expression profiling a cell or tissue sample that contains two or more RNAs of various abundances, comprising measuring hybridization signals of said sample to a plurality of oligonucleotide sequences, thereby determining the levels of said two or more RNAs in said sample and, where a RNA is transcribed from a transcription unit that has a set of splice variants, determining the total level of the set of splice variants, wherein said plurality is provided by the oligonucleotide library of claim 9 or a subset thereof.

29.-30. (cancelled)

31. (withdrawn) The oligonucleotide library of claim 29, wherein said transcriptome is rat transcriptome.

32. (withdrawn) The oligonucleotide library of claim 29, wherein said transcriptome is a mouse transcriptome.

33.- 43. (cancelled)

44. (withdrawn) A method for expression profiling a cell or tissue sample that contains two or more RNAs of various abundances, comprising measuring hybridization signals of said sample to a plurality of oligonucleotide sequences, thereby determining the levels of said two or more RNAs in said sample

and, where a RNA is transcribed from a transcription unit that has a set of splice variants, determining the total level of the set of splice variants, wherein said plurality is provided by the oligonucleotide library of claim 29 or a subset thereof.

45. (withdrawn) The method of claim 44, wherein said hybridization signals are obtained from a nucleotide chip.

46. (withdrawn) The method of claim 44, wherein said hybridization signals are obtained from an electrophoresis gel.

47. (withdrawn) A method for expression profiling a cell or tissue sample that contains two or more RNAs of various abundances, comprising measuring hybridization signals of said sample to a plurality of oligonucleotide sequences, thereby determining the levels of said two or more RNAs in said sample and, where a RNA is transcribed from a transcription unit that has a set of splice variants, determining the total level of the set of splice variants, wherein said plurality is provided by the oligonucleotide library of claim 33 or a subset thereof.

48. (withdrawn) The method of claim 47, wherein said hybridization signals are obtained from a nucleotide chip.

49. (withdrawn) The method of claim 47, wherein said hybridization signals are obtained from an electrophoresis gel.

50. (withdrawn) A method for expression profiling a cell or tissue sample that contains two or more RNAs of various abundances, comprising measuring hybridization signals of said sample to a plurality of oligonucleotide sequences, thereby determining the levels of said two or more RNAs in said sample and, where a RNA is transcribed from a transcription unit that has a set of splice variants, determining the total level of the set of splice variants, wherein said plurality is provided by the oligonucleotide library of claim 34 or a subset thereof.

51. (withdrawn) The method of claim 50, wherein said hybridization signals are obtained from a nucleotide chip.

52. (withdrawn) The method of claim 50, wherein said hybridization signals are obtained from an electrophoresis gel.

53. (withdrawn) A method for expression profiling a cell or tissue sample that contains two or more RNAs of various abundances, comprising measuring hybridization signals of said sample to a plurality of oligonucleotide sequences, thereby determining the levels of said two or more RNAs in said sample and, where a RNA is transcribed from a transcription unit that has a set of splice variants, determining the total level of the set of splice variants, wherein said plurality is provided by the oligonucleotide library of claim 36 or a subset thereof.

54. (withdrawn) The method of claim 53, wherein said hybridization signals are obtained from a nucleotide chip.

55. (withdrawn) The method of claim 53, wherein said hybridization signals are obtained from an electrophoresis gel.

56. (withdrawn) A method for expression profiling a cell or tissue sample that contains two or more RNAs of various abundances, comprising measuring hybridization signals of said sample to a plurality of oligonucleotide sequences, thereby determining the levels of said two or more RNAs in said sample and, where a RNA is transcribed from a transcription unit that has a set of splice variants, determining the total level of the set of splice variants, wherein said plurality is provided by the oligonucleotide library of claim 37 or a subset thereof.

57. (withdrawn) The method of claim 56, wherein said hybridization signals are obtained from a nucleotide chip.

58. (withdrawn) The method of claim 56, wherein said hybridization signals are obtained from an electrophoresis gel.

59. (withdrawn) A double stranded RNA molecule based on an oligonucleotide selected from an oligonucleotide library for detecting messenger RNAs that populate a transcriptome, wherein the transcriptome comprises messenger RNAs transcribed from a multiplicity of transcription units that populate a genome, wherein the library comprises a plurality of oligonucleotides, wherein each oligonucleotide in the plurality is capable of hybridizing selectively to a set of messenger RNAs transcribed from a given transcription unit of the genome, wherein at least one transcription unit of the genome encodes one or more messenger RNA splice variants, wherein the double-stranded RNA molecule comprises no more than 30 basepairs, wherein the double-stranded RNA molecule can interfere with translation of an mRNA.

60. (withdrawn) An antisense molecule based on an oligonucleotide selected from an oligonucleotide library for detecting messenger RNAs that populate a transcriptome, wherein the transcriptome comprises messenger RNAs transcribed from a multiplicity of transcription units that populate a genome, wherein the library comprises a plurality of oligonucleotides, wherein each oligonucleotide in the plurality is capable of hybridizing selectively to a set of messenger RNAs transcribed from a given transcription unit of the genome, wherein at least one transcription unit of the genome encodes one or more messenger RNA splice variants, wherein the antisense molecule comprises no more than 30 bases, wherein the double-stranded RNA molecule can interfere with translation of an mRNA.

61. (Currently amended) An oligonucleotide library for detecting messenger RNAs of a transcriptome or a sub transcriptome comprising a plurality of oligonucleotides each including a unique sequence shared by a set of RNA splice variants produced from a transcription unit transcribed in the transcriptome or the sub transcriptome, wherein said unique sequence is selected such that ~~an~~ each oligonucleotide of said plurality of oligonucleotides ~~selectively~~ hybridizes to ~~one~~ a set of RNA splice variants produced from only one transcription unit of the transcriptome or the sub transcriptome.

62. (Previously added) The oligonucleotide library of claim 61, wherein the transcriptome is a human transcriptome.

63. (Previously added) The oligonucleotide library of claim 61, wherein the sub transcriptome is of a specific tissue.

64. (Previously added) The oligonucleotide library of claim 61, wherein the sub transcriptome is of a pathological tissue.

65. (Previously added) The oligonucleotide library of claim 64, wherein said pathological tissue is cancer tissue.

66. (Previously added) The oligonucleotide library of claim 61, wherein the sub transcriptome is of a specific developmental stage.

67. (Previously added) The oligonucleotide library of claim 61, wherein the transcriptome is derived from an individual suffering from a disorder.

68. (Previously added) The oligonucleotide library of claim 67, wherein said disorder is cancer.

69. (Previously added) A DNA microarray having attached thereon the oligonucleotide library of claim 61.

70. (Previously added) A DNA microarray having attached thereon the oligonucleotide library of claim 62.

71. (Previously added) A DNA microarray having attached thereon the oligonucleotide library of claim 64.

72. (Previously added) A DNA microarray having attached thereon the oligonucleotide library of claim 65.

73. (Previously added) A DNA microarray having attached thereon the oligonucleotide library of claim 66.

74. (Previously added) A DNA microarray having attached thereon the oligonucleotide library of claim 67.